Claims

1. Method for detecting a microorganism contamination in a culture of eukaryotic cells to be used for gene expression profiling, the method comprising:
   (a) providing a microarray which has attached on its surface
      (a.1) at least one nucleic acid probe representing a gene of a eukaryotic cell and
      (a.2) at least one nucleic acid probe representing a gene of a microorganism,
   (b) preparing nucleic acid targets from said culture by means of a primer mixture suitable for amplifying said at least one gene of a eukaryotic cell and said at least one gene of a microorganism,
   (c) contacting the microarray of step (a) with the nucleic acid targets of step (b) to permit selective hybridization between the nucleic acid targets and their complementary nucleic acid probes on the microarray
   and
   (d) detecting said hybridization thereby detecting a microorganism contamination and, optionally, detecting the expression of genes specific for the eukaryotic cell.

2. The method according to claim 1, the method comprising an additional step:
   (e) comparing the gene expression of contaminated eukaryotic cells with the gene expression of non-contaminated eukaryotic cells.

3. The method according to claim 1 or 2, wherein the microorganism belongs to the class of mollicutes.

4. The method according to any of claims 1 to 3, wherein the mollicutes comprise the genera Mycoplasma, Ureaplasma, Acholeplasma and Spiroplasma.

5. The method according to any of claims 1 to 4, wherein the genus is Mycoplasma.

6. The method according to any of claims 1 to 5, wherein the nucleic acid probe representing a gene of the microorganism and the primer specific for said microorganism comprises a nucleic acid sequence of the 16S or 23S rRNA gene, preferably the 16S or 23S rRNA of mycoplasma.

7. The method according to claim 6, wherein said nucleic acid sequence of contains a sequence as defined by SEQ ID NOs: 1, 3, 4 or 5.

8. The method according to any of claims 1 to 7, wherein the preparing of a nucleic acid target sample in step (b) of claim 1 includes an in vitro transcription reaction.

9. The method according to claim 8, wherein the in vitro transcription is mediated by the use of primers containing the sequence of the T7 promoter, the T3 promoter or the SP6 promoter.

10. The method according to claim 9, wherein the promoter is the T7 promoter as defined by SEQ ID NO:2.

11. The method according to any of claims 1 to 10, wherein the eukaryotic cells are mammalian cells.

12. The method according to claim 11, wherein the mammalian cells are human cells.

13. A microarray which has attached on its surface
(a.1) at least one nucleic acid probe representing a gene of a eukaryotic cell and
(a.2) at least one nucleic acid probe representing a gene of a microorganism.

14. The microarray according to claim 13, wherein the nucleic acid probe in (a.2) comprises a sequence of the 16S rRNA gene, preferably of mycoplasma.

15. The microarray according to claim 14, wherein the sequence is defined by SEQ ID NO:1.

16. A diagnostic kit for detecting the presence of a microorganism in a cell culture, the kit containing a microarray as defined in any of claims 13 to 15, a suitable primer mixture, suitable enzymes, optionally labelled rNTPs, and a positive template control.

17. Method for analyzing the effect of a microorganism contamination on the gene expression of eukaryotic cells, the method comprising:
(a) providing a microarray which has attached on its surface

(a.1) at least one nucleic acid probe representing a gene of a eukaryotic cell and

(a.2) at least one nucleic acid probe representing a gene of a microorganism,

(b) preparing nucleic acid targets from the cell culture by means of a primer mixture suitable for amplifying said at least one gene of a eukaryotic cell and said at least one gene of a microorganism,

(c) contacting the microarray of step (a) with the nucleic acid targets of step (b) to permit selective hybridization between the nucleic acid targets and their complementary nucleic acid probes on the microarray

(d) detecting said hybridization thereby detecting the expression of genes specific a eukaryotic cells and detecting said microorganism contamination

and

(e) comparing the gene expression of contaminated eukaryotic cells with the gene expression of non-contaminated eukaryotic cells, wherein an altered expression of one or more genes is indicative of an effect of the microorganism on the expression of said genes.

18. Method for testing the suitability of a culture of eukaryotic cells for gene expression profiling by detecting the absence or presence of a microorganism, the method comprising:

(a) providing a microarray which has attached on its surface

(a.1) at least one nucleic acid probe representing a gene of a eukaryotic cell and

(a.2) at least one nucleic acid probe representing a gene of said microorganism,

(b) preparing nucleic acid targets from the cell culture by means of a primer mixture suitable for amplifying said at least one gene of a eukaryotic cell and at said least one gene of a microorganism,

(c) contacting the microarray of step (a) with the nucleic acid targets of step (b) to permit selective hybridization between the nucleic acid targets and their complementary nucleic acid probes on the microarray, and

(d) detecting said hybridization thereby detecting the absence or presence of a microorganism, wherein the absence indicates the suitability of said cell culture for gene expression profiling.

19. The method according to claim 18, wherein the method comprises an additional step:

(f) using the microarray of step c) for gene expression profiling provided the absence of a microorganism has been detected.

20. Use of a primer comprising the nucleic acid sequence complementary to the target region of a microorganism for detecting a microorganism contamination in a culture of eukaryotic cells to be used for gene expression profiling.

21. Use of a primer comprising the nucleic acid sequence complementary to the target region of a microorganism for analyzing the effect of a microorganism contamination on the gene expression of eukaryotic cells.

22. Use of a primer comprising the nucleic acid sequence complementary to the target region of a microorganism for testing the suitability of a culture of eukaryotic cells for gene expression profiling by detecting the absence or presence of a microorganism.

23. The use according to any of claims 20 to 22, wherein the target region of a microorganism is 16S rRNA, preferably the 16S rRNA of Mycoplasma.

24. The use according to any of claims 20 to 23, wherein the gene expression profiling is done by using a microarray as defined in any of claims 13 to 15.

25. Use of a microarray as defined in any of claims 13 to 15 for detecting a microorganism contamination in a culture of eukaryotic cells to be used for gene expression profiling.

26. Use of a culture of eukaryotic cells, an extract or fraction thereof, for gene expression profiling, characterized in that said culture of eukaryotic cells is tested for suitability for gene expression by a method as defined in claim 18 or 19.